

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:01:01 ; Search time 258.605 Seconds
(without alignments)
72.265 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWFWQRMRKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

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3: /cgn2_6/ptodata/1/paa/us07 COMB.pcp.*

4: /cgn2_6/ptodata/1/paa/us08 COMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	1	PCT-US00-05097-54
2	92	100.0	16	1	PCT-US01-27692A-122
3	92	100.0	16	1	PCT-US01-51600-3
4	92	100.0	16	1	PCT-US02-02837A-2
5	92	100.0	16	1	PCT-US02-05804-29
6	92	100.0	16	1	PCT-US02-05829-29
7	92	100.0	16	1	PCT-US02-11754-3
8	92	100.0	16	1	PCT-US02-13609-21
9	92	100.0	16	1	PCT-US02-20337-1
10	92	100.0	16	1	PCT-US02-22324-14
11	92	100.0	16	1	PCT-US02-27421-2
12	92	100.0	16	1	PCT-US02-27836-55
13	92	100.0	16	1	PCT-US02-30094-5
14	92	100.0	16	1	PCT-US02-33511-113
15	92	100.0	16	1	PCT-US03-01529-10
16	92	100.0	16	1	PCT-US03-01529-14
17	92	100.0	16	1	PCT-US03-02358-71
18	92	100.0	16	1	PCT-US03-02358-75
19	92	100.0	16	1	PCT-US03-02358-75
20	92	100.0	16	1	PCT-US03-02358-75
21	92	100.0	16	1	PCT-US03-02358-75
22	92	100.0	16	1	PCT-US03-02358-75
23	92	100.0	16	1	PCT-US03-02358-75
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26	92	100.0	16	1	PCT-US03-02358-75
27	92	100.0	16	1	PCT-US03-02358-75
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41	92	100.0	16	1	PCT-US03-02358-75
42	92	100.0	16	1	PCT-US03-02358-75
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44	92	100.0	16	1	PCT-US03-02358-75
45	92	100.0	16	1	PCT-US03-02358-75

ALIGNMENTS

RESULT 1
PCT-US00-05097-54
; Sequence 54, Application PC/TUS0005097
; GENERAL INFORMATION:
; APPLICANT: Washington University
; TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS
; TITLE OF INVENTION: FOR USING SAME
; FILE REFERENCE: 49054-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05097
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: 60/122,757
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: 60/151,291
; PRIOR FILING DATE: 1999-08-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT

; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
PCT-US00-05097-54

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
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Db 1 RQIKWIFQNRRMKWK 16

RESULT 2
PCT-US01-27692A-122
; Sequence 122, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US01-27692A-122

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
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Db 1 RQIKWIFQNRRMKWK 16

RESULT 3
PCT-US01-51600-3
; Sequence 3, Application PC/TUS0151600
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the Leland
; APPLICANT: Stanford Junior University
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Iachemia
; FILE REFERENCE: 58600-8209.W000
; CURRENT APPLICATION NUMBER: PCT/US01/51600
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Drosophila antennapedia homeodomain-derived
; OTHER INFORMATION: carrier peptide
PCT-US01-51600-3

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
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Db 1 RQIKWIFQNRRMKWK 16

RESULT 4
PCT-US02-02837A-2
; Sequence 2, Application PC/TUS0202837A
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: Rabinovich, Peter
; APPLICANT: Bray-Ward, Patricia
; APPLICANT: Ward, David
; TITLE OF INVENTION: PEPTIDES FOR FACILITATING COMPOSITE RECEPTOR EXPRESSION AND TRANS
; FILE REFERENCE: 044574-5079WO
; CURRENT APPLICATION NUMBER: PCT/US02/02837A
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/265,624
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
PCT-US02-02837A-2

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
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Db 1 RQIKWIFQNRRMKWK 16

RESULT 5
PCT-US02-05804-29
; Sequence 29, Application PC/TUS0205804
; GENERAL INFORMATION:
; APPLICANT: Rothbard, Jonathan B.
; APPLICANT: Wender, Paul A.
; APPLICANT: McGrane, P. Leo
; APPLICANT: Sista, Lalitha V.S.
; APPLICANT: Kirschberg, Thorsten A.
; APPLICANT: CellGate, Inc.
; TITLE OF INVENTION: Compositions and Methods for Enhancing
; TITLE OF INVENTION: Drug Delivery Across and Into Ocular Tissues
; FILE REFERENCE: 019801-000240PC
; CURRENT APPLICATION NUMBER: PCT/US02/05804
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 09/792,480
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antennapedia homeodomain region residues 43-58
PCT-US02-05804-29

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRRMKWK 16
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Db 1 RQIKWIFQNRRMKWK 16

RESULT 6
PCT-US02-05829-29
; Sequence 29, Application PC/TUS0205829
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 14:03:57 ; Search time 37.9535 Seconds
(without alignments)
73.895 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWFOQRNRKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286997 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	92	100.0	16	1	PCT-US05-01251-5
3	92	100.0	16	1	PCT-US05-01771-13
4	92	100.0	16	1	PCT-US05-05458-9
5	92	100.0	16	1	PCT-US04-36200-7
6	92	100.0	16	1	PCT-US05-11741-4
7	92	100.0	16	1	PCT-US05-16746-1
8	92	100.0	16	1	PCT-US05-18985-6
9	92	100.0	16	1	PCT-US04-06511A-10
10	92	100.0	16	5	US-09-959-873-10
11	92	100.0	16	6	US-10-930-313-57
12	92	100.0	16	6	US-10-156-570B-21
13	92	100.0	16	6	US-10-909-769-6
14	92	100.0	16	6	US-10-909-769-8
15	92	100.0	16	6	US-10-927-282A-43
16	92	100.0	16	6	US-10-700-971C-1
17	92	100.0	16	6	US-10-500-671A-10
18	92	100.0	16	6	US-10-500-671A-14
19	92	100.0	16	6	US-10-878-175B-20
20	92	100.0	16	6	US-10-840-060-1
21	92	100.0	16	6	US-10-451-314A-12
22	92	100.0	16	6	US-10-201-389B-14
23	92	100.0	16	6	US-10-991-286A-31
24	92	100.0	16	6	US-10-991-286A-49
25	92	100.0	16	6	US-10-533-124-4

26	92	100.0	16	6	US-10-985-426-1	Sequence 1, Appli
27	92	100.0	16	6	US-10-985-426-19	Sequence 19, Appl
28	92	100.0	16	6	US-10-865-538-21	Sequence 21, Appl
29	92	100.0	16	6	US-10-983-493-6	Sequence 6, Appli
30	92	100.0	16	6	US-10-535-780-5	Sequence 5, Appli
31	92	100.0	16	6	US-10-899-912A-24	Sequence 24, Appl
32	92	100.0	16	6	US-10-899-912A-42	Sequence 42, Appl
33	92	100.0	16	6	US-10-740-365-29	Sequence 29, Appl
34	92	100.0	16	6	US-10-083-960B-29	Sequence 29, Appl
35	92	100.0	16	6	US-10-462-138A-10	Sequence 10, Appl
36	92	100.0	16	6	US-10-923-112A-20	Sequence 20, Appl
37	92	100.0	16	6	US-10-229-915A-2	Sequence 2, Appli
38	92	100.0	16	6	US-10-287-196A-6	Sequence 6, Appli
39	92	100.0	16	7	US-11-027-967-2	Sequence 2, Appli
40	92	100.0	16	7	US-11-035-714-5	Sequence 5, Appli
41	92	100.0	16	7	US-11-041-103-13	Sequence 13, Appl
42	92	100.0	16	7	US-11-060-005-32	Sequence 32, Appl
43	92	100.0	16	7	US-11-102-432-2	Sequence 2, Appli
44	92	100.0	16	7	US-11-101-463-11	Sequence 11, Appl
45	92	100.0	16	7	US-11-127-903-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

PCT-US04-35009-7
; Sequence 7, Application PC/TUS0435009
; GENERAL INFORMATION:
; APPLICANT: Wake Forest University Health Sciences
; TITLE OF INVENTION: NON-VIRAL DELIVERY OF COMPOUNDS TO THE MITOCHONDRIA
; FILE REFERENCE: 9151-37WO
; CURRENT APPLICATION NUMBER: PCT/US04/35009
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,892
; PRIOR FILING DATE: 2003-10-24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US04-35009-7

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWFOQRNRKWK 16
DB 1 RQIKWFOQRNRKWK 16

RESULT 2

PCT-US05-01251-5
; Sequence 5, Application PC/TUS0501251
; GENERAL INFORMATION:
; APPLICANT: LAUDANNA, CARLO
; APPLICANT: BUTCHER, EUGENE C.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF RHOA SIGNALING
; FILE REFERENCE: STAN-346WO
; CURRENT APPLICATION NUMBER: PCT/US05/01251
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/537,142
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: H. sapien
PCT-US05-01251-5

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Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 3
PCT-US05-01771-13
; Sequence 13, Application PC/TUS0501771
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; APPLICANT: Bao, Gang
; APPLICANT: Nitin, Nitin
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection
; FILE REFERENCE: 820701-2820
; CURRENT APPLICATION NUMBER: PCT/US05/01771
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/179,730
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/300,672
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/303,258
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
PCT-US05-01771-13

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 4
PCT-US05-05458-9
; Sequence 9, Application PC/TUS0505458
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION USING TRIMSALPHA
; FILE REFERENCE: DFN-058PC
; CURRENT APPLICATION NUMBER: PCT/US05/05458
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/548,139
; PRIOR FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila
PCT-US05-05458-9

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 RQIKWQNRRMKWKK 16

RESULT 5
PCT-US04-36200-7
; Sequence 7, Application PC/TUS0436200
; GENERAL INFORMATION:
; APPLICANT: THE CBR INSTITUTE FOR BIOMEDICAL RESEARCH, INC.
; APPLICANT: LIEBERMAN, JUDY
; APPLICANT: HAMAR, PETER
; TITLE OF INVENTION: METHODS FOR TREATING AND PREVENTING ISCHEMIA-REPERFUSION
; TITLE OF INVENTION: INJURY USING RNA INTERFERING AGENTS
; FILE REFERENCE: 03393-55221
; CURRENT APPLICATION NUMBER: PCT/US04/36200
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,172
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila sp.
PCT-US04-36200-7

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
DB 1 RQIKWQNRRMKWKK 16

RESULT 6
PCT-US05-11741-4
; Sequence 4, Application PC/TUS0511741
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: Pandol, Stephen J
; APPLICANT: Gukovskaya, Anna
; APPLICANT: Yazbeck, Moussa
; APPLICANT: Eibl, Guido
; APPLICANT: Boros, Laszlo G
; APPLICANT: Sato, Akihiko
; TITLE OF INVENTION: COMPOSITIONS COMPRISING PLANT-DERIVED POLYPHENOLIC COMPOUNDS AND
; TITLE OF INVENTION: INHIBITORS OF REACTIVE OXYGEN SPECIES AND METHODS OF USING
; FILE REFERENCE: 034044.021.1
; CURRENT APPLICATION NUMBER: PCT/US05/11741
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: US 10/260,609
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/562,315
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 10/824,597
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
PCT-US05-11741-4

Query Match      100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:20:28 ; Search time 18.6047 Seconds
(without alignments)
82.746 Million cell updates/sec

Title: US-10-071-512A-2
Perfect score: 92
Sequence: 1 RQIKIWFQNRRMKWKK 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	33	2 S57235	antennapedia prote
2	92	100.0	42	2 I65241	homeotic protein H
3	92	100.0	45	2 PC1216	homeotic protein D
4	92	100.0	48	2 I5439	homeobox protein -
5	92	100.0	66	2 S1538	homeotic protein H
6	92	100.0	66	2 S1536	homeotic protein H
7	92	100.0	71	2 JC1161	homeotic protein 3
8	92	100.0	71	2 A60084	homeotic protein H
9	92	100.0	74	2 D34510	homeotic protein H
10	92	100.0	75	2 S58852	homeotic protein S
11	92	100.0	75	2 I51341	homeo box protein
12	92	100.0	76	2 C43559	homeotic protein R
13	92	100.0	78	2 I51342	homeo box protein
14	92	100.0	81	2 B29585	homeotic protein H
15	92	100.0	81	2 S47605	homeotic protein H
16	92	100.0	82	2 S50066	homeotic protein H
17	92	100.0	83	2 S47603	homeotic protein H
18	92	100.0	83	2 A34510	homeotic protein H
19	92	100.0	86	2 S08303	homeotic protein H
20	92	100.0	86	2 J70489	homeotic protein Z
21	92	100.0	87	2 S00589	homeotic protein H
22	92	100.0	87	2 A03317	homeotic protein M
23	92	100.0	88	2 S08639	homeotic protein z
24	92	100.0	96	2 A05266	homeotic protein H
25	92	100.0	96	2 C27176	homeotic protein H
26	92	100.0	97	2 A24779	homeotic protein m
27	92	100.0	103	2 A32167	homeotic protein H
28	92	100.0	105	2 S47602	homeotic protein H
29	92	100.0			

30	92	100.0	105	2 A27471	homeotic protein R
31	92	100.0	106	2 S36448	homeotic protein s
32	92	100.0	107	2 B61045	homeotic protein T
33	92	100.0	113	2 T10775	homeobox protein -
34	92	100.0	118	2 A24777	homeotic protein H
35	92	100.0	118	2 J70273	homeotic protein H
36	92	100.0	118	2 B24777	homeotic protein M
37	92	100.0	119	2 A03314	homeotic protein m
38	92	100.0	138	2 S20087	homeotic protein b
39	92	100.0	148	2 PC4071	homeobox A5 protei
40	92	100.0	153	1 WJHU3C	homeotic protein H
41	92	100.0	153	1 WJMSX6	homeotic protein H
42	92	100.0	158	2 A27348	homeotic protein H
43	92	100.0	209	2 A43553	homeotic protein H
44	92	100.0	217	1 WJHU2C	homeotic protein H
45	92	100.0	217	1 WJMSX2	homeotic protein H

ALIGNMENTS

RESULT 1

S57235
antennapedia protein (clone pl105) - fruit fly (Drosophila pseudoobscura) (fragment)
C:Species: Drosophila pseudoobscura
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S57235
R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.
Genetics 133, 319-330, 1993
A>Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
A:Reference number: S57224
A:Accession: S57235
A:Molecule type: DNA
A:Residues: 1-33 <RAN>
A:Cross-references: EMBL:X77711
C:Genetics:
A:Gene: FlyBase:Antp
A:Cross-references: FlyBase:FBgn0012693
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWKK 16
DB 7 RQIKIWFQNRRMKWKK 22

RESULT 2

I65241
homeotic protein Hox-A - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Aug-2004
C:Accession: I65241
R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
A>Title: Cloning of rat homeobox genes.
A:Reference number: I52340; MUID:95217128; PMID:7702549
A:Accession: I65241
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S76290; NID:g913077
C:Genetics:
A:Gene: Hox-A; Hox-1
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 42;

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Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 25 RQIKWQNRRMKWKK 40

RESULT 3
PC1216
homeotic protein DdHx1 - planarian (Dugesia tigrina) (fragment)
C:Species: Dugesia tigrina
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C:Accession: PC1216
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich, G.
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JCI1386; MUID:1359988
A:Accession: PC1216
A:Molecule type: DNA
A:Residues: 1-45 <OLI>
A:Cross-references: UNIPROT:P91714; EMBL:X66822
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 30 RQIKWQNRRMKWKK 45

RESULT 4
IS1439
homeobox protein - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C:Accession: IS1439
R:Leroy, P.; DeRobertis, E.M.
Dev. Dyn. 194, 21-32, 1992
A:Title: Effects of lithium chloride and retinoic acid on the expression of genes from the homeobox family.
A:Reference number: IS1439; MUID:93043517; PMID:1384809
A:Accession: IS1439
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-48 <LER>
A:Cross-references: UNIPROT:P31256; GB:M91587; NID:g214257; PIDN:AAA49750.1; PID:g214258
C:Genetics:
A:Gene: Hox2.2
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-27/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 92; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 12 RQIKWQNRRMKWKK 27

RESULT 5
S15538
homeotic protein Hox A6 - human (fragment)
N:Alternate names: homeotic protein Hox 1B
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C:Accession: S15538
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Strotmann, R.
Gene 114, 179-186, 1992
A:Title: Homeobox-containing genes in the newt are organized in clusters similar to other vertebrates.
A:Reference number: JCI1161; MUID:92290273; PMID:1351019
A:Accession: JCI1161
A:Molecule type: DNA
A:Residues: 1-71 <BEL>
A:Cross-references: UNIPROT:P31262; GB:M84001
C:Genetics:

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Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15538
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-66 <BON>
A:Cross-references: UNIPROT:P31267
C:Genetics:
A:Gene: GDB:HOXA6
A:Cross-references: GDB:120648; OMIM:142951
A:Map position: 7p15.3-7p15.3
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 43 RQIKWQNRRMKWKK 58

RESULT 6
S15536
homeotic protein Hox A7 - human (fragment)
N:Alternate names: homeotic protein Hox 1A
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C:Accession: S15536
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Strotmann, R.
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15536
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-66 <BON>
A:Cross-references: UNIPROT:P31268
C:Genetics:
A:Gene: GDB:HOXA7
A:Cross-references: GDB:120647; OMIM:142950
A:Map position: 7p15.3-7p15.3
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 92; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWQNRRMKWKK 16
Db 43 RQIKWQNRRMKWKK 58

RESULT 7
JC1161
homeotic protein 3.4 - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-2004
C:Accession: JC1161
R:Belleville, S.; Beauchemin, M.; Tremblay, M.; Noiseux, N.; Savard, P.
Gene 114, 179-186, 1992
A:Title: Homeobox-containing genes in the newt are organized in clusters similar to other vertebrates.
A:Reference number: JCI1161; MUID:92290273; PMID:1351019
A:Accession: JCI1161
A:Molecule type: DNA
A:Residues: 1-71 <BEL>
A:Cross-references: UNIPROT:P31262; GB:M84001
C:Genetics:

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:08:33 ; Search time 86.3256 Seconds
(without alignments)
94.911 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKWQNRRMKWKK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	33	Q86FU0	Q86fu0 drosophila
2	92	100.0	39	Q57368	Q57368 brachydanio
3	92	100.0	42	Q80WH6	Q80wh6 rattus sp.
4	92	100.0	43	Q57359	Q57359 brachydanio
5	92	100.0	44	Q6L873	Q6l873 lampetra la
6	92	100.0	46	Q9PVR9	Q9pvr9 oryzias lat
7	92	100.0	47	Q6IT83	Q6it83 oncopeltus
8	92	100.0	48	1 HXB6 XENLA	P31256 xenopus lae
9	92	100.0	49	1 HXA5 SHEEP	Q28599 ovis aries
10	92	100.0	51	Q23743	Q23743 ctenodrilus
11	92	100.0	51	Q26407	Q26407 ctenodrilus
12	92	100.0	51	Q27413	Q27413 ctenodrilus
13	92	100.0	51	Q7JPR7	Q7jpr7 ctenodrilus
14	92	100.0	57	Q9PVR8	Q9pvr8 oryzias lat
15	92	100.0	58	Q25208	Q25208 junonia coe
16	92	100.0	58	Q9Y188	Q9y188 priapulus c
17	92	100.0	58	Q57362	Q57362 brachydanio
18	92	100.0	59	Q8WRM9	Q8wrn9 lithobius a
19	92	100.0	59	Q9NB42	Q9nb42 anopheles g
20	92	100.0	59	Q9PVR5	Q9pvr5 oryzias lat
21	92	100.0	60	Q77139	Q77139 archegozete
22	92	100.0	60	Q77143	Q77143 archegozete
23	92	100.0	60	Q80WH4	Q80wh4 rattus sp.
24	92	100.0	60	Q80WH7	Q80wh7 rattus sp.
25	92	100.0	60	Q8QGL2	Q8qgl2 petromyzon
26	92	100.0	60	Q8QGL3	Q8qgl3 petromyzon
27	92	100.0	60	Q8QGL5	Q8qgl5 petromyzon
28	92	100.0	60	Q8QGL6	Q8qgl6 petromyzon
29	92	100.0	60	Q8QGL7	Q8qgl7 petromyzon
30	92	100.0	60	Q8QGL8	Q8qgl8 petromyzon
31	92	100.0	61	Q27910	Q27910 polyandroca

32 92 100.0 63 2 Q77138 archegozete
33 92 100.0 63 2 Q8MXB2 holopneuste
34 92 100.0 66 2 Q57356 brachydanio
35 92 100.0 69 2 Q9BMF7 haliotis ae
36 92 100.0 69 2 Q9U9T4 nereis vire
37 92 100.0 70 2 Q967W5
38 92 100.0 70 2 Q801B4
39 92 100.0 71 1 HXA7 SHEEP
40 92 100.0 71 1 HXC5 NOTVI
41 92 100.0 71 2 Q6EBC8
42 92 100.0 71 2 Q9PVS1
43 92 100.0 71 2 Q9PVS3
44 92 100.0 73 2 Q86D93
45 92 100.0 73 2 Q9Y186

ALIGNMENTS

RESULT 1
Q86FU0 PRELIMINARY; PRT; 33 AA.
AC Q86FU0;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Antennapedia complex (Fragment).
GN Name=ANT-C;
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292933; PubMed=8099892;
RA Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,
RA Kaufman T.C.;
RT "Structural changes in the antennapedia complex of Drosophila
RT pseudoobscura";
RL Genetics 134:319-330(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; S63455; AAP13946.1; -.
DR HSSP; P02833; 1HOM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR PRINTS; PRO0024; HOMEOBOX.
DR Probom; PD000010; Homeobox; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3963 MW; D78E37ED81PD45DF CRC64;

Query Match 100.0%; Score 92; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
|||||
Db 7 RQIKWQNRRMKWKK 22

RESULT 2
Q57368 PRELIMINARY; PRT; 39 AA.
AC Q57368;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE HoxC5 protein (Fragment).
GN Name=hoxc5; Synonyms=hoxc5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; Y14539; CA74874.1; -.
DR HSP; P02833; IHOM.
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E58860 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKWK 16
|||||
DB 14 RQIKWIFQNRKMKWK 29

RESULT 3
Q80WH6 PRELIMINARY; PRT; 42 AA.
AC Q80WH6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hox-A|Hox-1 (Fragment).
GN Name=Hox-A|Hox-1;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217128; PubMed=7702549;
RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
RT "Cloning of rat homeobox genes."
RL Biochem. Genet. 32:351-360(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; S76290; AAP31864.1; -.
DR HSP; P02833; IHOM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 5494 MW; 38E5153B92216FE9 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKWK 16
|||||
DB 25 RQIKWIFQNRKMKWK 40

RESULT 4
O57359 PRELIMINARY; PRT; 43 AA.
AC O57359;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hoxa5 protein (Fragment).
GN Name=hox5b; Synonyms=hoxa5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; Y14526; CA74861.1; -.
DR HSP; P02833; IHOM.
DR ZFIN; ZDB-GENE-000823-6; hox5b.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 100.0%; Score 92; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRKMKWK 16
|||||
DB 10 RQIKWIFQNRKMKWK 25

RESULT 5
Q6L8J3 PRELIMINARY; PRT; 44 AA.
AC Q6L8J3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LjHox7m Homeobox (Fragment).
GN Name=LjHox7m;
OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:07:33 ; Search time 89.6744 Seconds
(without alignments)
69.007 Million cell updates/sec

Title: US-10-071-512A-2

Perfect score: 92

Sequence: 1 RQIKIWFQNRRMKWKK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	16	2 AAW45974	AAW45974 Cysteine
2	92	100.0	16	2 AAW33407	AAW33407 Peptide 4
3	92	100.0	16	2 AAW33410	AAW33410 D-form pe
4	92	100.0	16	2 AAW82958	AAW82958 Oestrogen
5	92	100.0	16	2 AAW56397	AAW56397 Preferred
6	92	100.0	16	2 AAW71270	AAW71270 Antennape
7	92	100.0	16	2 AAW71316	AAW71316 Antennape
8	92	100.0	16	2 AAW30508	AAW30508 Drosophil
9	92	100.0	16	2 AAW91046	AAW91046 Internali
10	92	100.0	16	2 AAW52102	AAW52102 Peptide f
11	92	100.0	16	2 AAY00859	AAY00859 Peptide p
12	92	100.0	16	2 AAY13509	AAY13509 Signal ee
13	92	100.0	16	3 AAY87920	AAY87920 Drosophil
14	92	100.0	16	3 AAW27060	AAW27060 Beta-cate
15	92	100.0	16	3 AAY93667	AAY93667 Peptide w
16	92	100.0	16	3 AAY67966	AAY67966 Carboxyfl
17	92	100.0	16	3 AAY93551	AAY93551 Amino aci
18	92	100.0	16	3 AAY55818	AAY55818 Signal ee
19	92	100.0	16	3 AAY71008	AAY71008 Drosophil
20	92	100.0	16	3 AAY51212	AAY51212 Antennape
21	92	100.0	16	3 AAY51167	AAY51167 Drosophil
22	92	100.0	16	3 AAB10343	AAB10343 Peptide A
23	92	100.0	16	3 AAB19251	AAB19251 Fragment
24	92	100.0	16	3 AAY93178	AAY93178 Protegrin
25	92	100.0	16	3 AAB35694	AAB35694 Peptide a

26	92	100.0	16	3 AAB22025	AAB22025 Membrane
27	92	100.0	16	3 AAB29423	AAB29423 ANTP pept
28	92	100.0	16	3 AAB03927	AAB03927 Internali
29	92	100.0	16	3 AAY93954	AAY93954 Peptide u
30	92	100.0	16	3 AAB29574	AAB29574 Antennape
31	92	100.0	16	3 ADE14785	ADE14785 Carrier m
32	92	100.0	16	3 ADE14761	ADE14761 Drosophil
33	92	100.0	16	4 AAB73091	AAB73091 Rheumatoi
34	92	100.0	16	4 AAB60004	AAB60004 Internali
35	92	100.0	16	4 AAB70753	AAB70753 Cell memb
36	92	100.0	16	4 AAE02974	AAE02974 Protein t
37	92	100.0	16	4 AAB60671	AAB60671 Antennape
38	92	100.0	16	4 AAU06064	AAU06064 Drosophil
39	92	100.0	16	4 AAB49914	AAB49914 HIF-1alph
40	92	100.0	16	4 AAB66996	AAB66996 Antennape
41	92	100.0	16	4 AAU00813	AAU00813 Fruit fly
42	92	100.0	16	4 AAE12205	AAE12205 Membrane
43	92	100.0	16	5 ABB78030	ABB78030 Peptide d
44	92	100.0	16	5 ABB78985	ABB78985 Cell pene
45	92	100.0	16	5 ABB78214	ABB78214 Amino aci

ALIGNMENTS

RESULT 1
AAW45974
ID AAW45974 standard; peptide; 16 AA.
XX AAW45974;
XX
DT 01-JUL-1998 (first entry)
XX
DE Cysteine protease inhibiting peptide for preventing cell death.
XX
KW Neuronal cell death; neurodegenerative disorder; inhibition;
KW Cysteine protease; cardiovascular; liver disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
XX
PN WO9735876-A1.
XX
PD 02-OCT-1997.
XX
PF 04-MAR-1997; 97WO-US004158.
XX
PR 04-MAR-1996; 96US-00610220.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Troy CM;
XX
WPI; 1997-489561/45.
XX
PT New cysteine protease inhibiting peptide(s) for preventing cell death -
PT in cases of neurodegenerative, cardiovascular and liver diseases, and
PT their peptidomimetics, and general method for identifying enzyme
PT inhibiting peptides.
XX
PS Claim 8; page 68; 112pp; English.
XX
CC This sequence represents a specifically claimed peptide of the formula: V
CC -(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if
CC n =1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n =3 or more, (AA1)n
CC = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if
CC m = 1, AA2 = Arg; if m =2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n =
CC Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'', any or all
CC of which may be absent, = agent able to direct the compound to a specific
CC cell. The peptides are inhibitors of cysteine proteases, specifically

CC interleukin-1 beta converting enzyme (ICE). They inhibit death of cells,
 CC particularly in humans, and can be used to treat neurodegenerative
 CC diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or
 CC Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke),
 CC cardiovascular disease and liver disorders. The peptides should be more
 CC specific than pseudosubstrate inhibitors

XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWQNRRMKWKK 16
 |||||
 DB 1 RQIKIWQNRRMKWKK 16

RESULT 2

ID AAW33407 standard; peptide; 16 AA.

XX AAW33407;

DT 27-AUG-2003 (revised)
 DT 17-MAR-1998 (first entry)

DE Peptide 43-58 of homeodomain Antp.

XX homeodomain; transcription factor; Antennapedia; Antp; vector;
 KW transfection; hydrophobic.

OS Unidentified.

PN WO9712912-A1.

PD 10-APR-1997.

PF 04-OCT-1996; 96WO-FR001553.

PR 05-OCT-1995; 95FR-00011714.

XX (CNRS) CNRS CENT NAT RECH SCI.

Chassaing G, Prochiantz A;

WPI; 1997-226166/20.

New peptide(s) of high hydrophobic amino acid content - useful as vectors
 for delivering peptides and nucleic acids to cells.

Claim 1; Page 7; 35pp; French.

New peptides are provided which are 16 amino acids long and which are
 analogues of the peptide corresponding to residues 43-58 of the
 Antennapedia transcription factor homeodomain (AntpHD). The peptides
 contain 6-10 hydrophobic amino acids. They have the general formula: X1-
 X2-X3-X4-X5-Trp-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-
 X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any
 alpha-amino acids, provided that: (1) the peptide contains 6-10
 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the
 natural Antp 43-58 sequence RQIKIWQNRRMKWKK (i.e. the present sequence)
 is excluded. Specific examples of these peptides are given in AAW33408 -
 AAW33416. The peptides are used as vectors for introducing into live
 cells compounds which affect cell function, esp. peptides and nucleic
 acids. They can cross cellular membranes and reach various cell
 compartments. They are as effective as helix 3 of a homeodomain peptide.
 (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKIWQNRRMKWKK 16
 |||||
 DB 1 RQIKIWQNRRMKWKK 16

RESULT 3

AAW33410
 ID AAW33410 standard; peptide; 16 AA.

XX AAW33410;

DT 17-MAR-1998 (first entry)

DE D-form peptide 43-58 of homeodomain Antp.

XX homeodomain; transcription factor; Antennapedia; Antp; vector;
 KW transfection; hydrophobic.

OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1..16
 FT /note= "all residues are D-form"

FT Modified-site 1
 FT /note= "in determining the ability of this sequence to be
 FT internalised in cells, a biotin-aminopentanoyl group was
 FT attached to the N-terminal"

PN WO9712912-A1.

PD 10-APR-1997.

PF 04-OCT-1996; 96WO-FR001553.

PR 05-OCT-1995; 95FR-00011714.

XX (CNRS) CNRS CENT NAT RECH SCI.

Chassaing G, Prochiantz A;

WPI; 1997-226166/20.

New peptide(s) of high hydrophobic amino acid content - useful as vectors
 for delivering peptides and nucleic acids to cells.

Disclosure; Page 7; 35pp; French.

New peptides are provided which are 16 amino acids long and which are
 analogues of the peptide corresponding to residues 43-58 of the
 Antennapedia transcription factor homeodomain (AntpHD). The peptides
 contain 6-10 hydrophobic amino acids. They have the general formula: X1-
 X2-X3-X4-X5-Trp-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-
 X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any
 alpha-amino acids, provided that: (1) the peptide contains 6-10
 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the
 natural Antp 43-58 sequence RQIKIWQNRRMKWKK (see AAW33407) is excluded.
 The present sequence (the D-form of the 43-58 peptide) is a specific
 example of the new peptides. The peptides are used as vectors for
 introducing into live cells compounds which affect cell function,
 especially peptides and nucleic acids. They can cross cellular membranes
 and reach various cell compartments. They are as effective as helix 3 of
 a homeodomain peptide

Sequence 16 AA;

Query Match 100.0%; Score 92; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKIWQNRRMKWKK 16
 |||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:07:33 ; Search time 151.326 Seconds
(without alignments)
69.007 Million cell updates/sec

Title: US-10-071-512A-3

Perfect score: 133
Sequence: 1 GWTLSAGYLLGKINKALAAAKKIL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	100.0	27	2	Aay00858 Peptide #
2	133	100.0	27	3	Aab17999 Membrane
3	133	100.0	27	3	Aab22024 Membrane
4	133	100.0	27	3	Aab29575 Transport
5	133	100.0	27	4	Aae02978 Hydrophob
6	133	100.0	27	4	Aae06072 Transport
7	133	100.0	27	4	Aae12488 Membrane
8	133	100.0	27	5	Aab78215 Amino aci
9	133	100.0	27	5	Aab73370 Exemplary
10	133	100.0	27	5	Aae22207 Transport
11	133	100.0	27	6	Abp72305 Transport
12	133	100.0	27	6	Aae35392 Transport
13	133	100.0	27	6	Abp43124 Human mem
14	133	100.0	27	6	Abp2915 Transport
15	133	100.0	27	7	Adg82623 Transport
16	133	100.0	27	7	Adg28015 Synthetic
17	133	100.0	27	7	Adj73523 Exemplary
18	133	100.0	27	7	Adl88651 Transport
19	133	100.0	27	7	Adl23664 Galanin (
20	133	100.0	27	8	Adh89687 Cell pene
21	133	100.0	27	8	Adj53157 CH1 delet
22	133	100.0	27	8	Adj52118 CH1 delet
23	133	100.0	27	8	Adj78885 Transport
24	133	100.0	27	8	Adk15590 Membrane
25	133	100.0	27	8	Ado26479 Galanin a

ALIGNMENTS

RESULT 1

AA00858

ID AAY00858 standard; peptide; 27 AA.

XX AC AAY00858;

XX DT 20-MAY-1999 (first entry)

XX DE Peptide #3 used in membrane-permeable construct.

XX KW Membrane-permeable construct; lipid membrane; membrane transport;
KW oligonucleotide delivery; cancer therapy; signal transduction; inhibitor;
KW gene therapy; transcription; translation; expression; replication.

XX OS Synthetic.

XX PN WO9905302-Al.

XX PD 04-FEB-1999.

XX PF 16-JUL-1998; 98WO-US014761.

XX PR 24-JUL-1997; 97US-0053678P.

XX PA (PEKE) PERKIN-ELMER CORP.

XX PI Langel U, Bartfai T, Pooga M, Valkna A, Saar K, Hallbrink M;

XX DR WPI; 1999-142952/12.

XX PT New membrane-permeable constructs - comprise a peptide linked by a labile bond to a nucleic acid analogue capable of hybridising with an intracellular polynucleotide.

XX PS Claim 5; Page 41; 60pp; English.

XX CC This sequence represents a peptide used in the construct of the invention. The construct is a membrane-permeable construct for transport across a lipid membrane, which comprises: (a) a nucleic acid analogue capable of hybridising with an intracellular polynucleotide (PN); (b) a peptide; and (c) a labile bond linking the nucleic acid analogue and the peptide. The membrane-permeable constructs can be used for delivery of oligonucleotides, nucleic acids and nucleic acid analogues into cells. They can be used for e.g. cancer therapy, signal transduction studies, identifying new intracellular drug targets or gene therapy. They can also be used for selectively inhibiting DNA transcription, RNA translation, RNA or DNA expression, DNA replication, or an DNA or RNA regulatory function of preselected DNA or RNA sequences in a living cell

26	133	100.0	27	8	ADM97018
27	133	100.0	27	8	ADO43344
28	133	100.0	27	8	ADO80842
29	133	100.0	27	8	ADO60192
30	133	100.0	27	8	ADR00873
31	133	100.0	27	8	ADSI17605
32	133	100.0	28	8	ADK39821
33	133	100.0	28	8	ADK39821
34	131	98.5	27	8	ADH89695
35	128	96.2	27	8	ADH89696
36	127	95.5	27	8	ADO25261
37	126	94.7	27	7	ADC22458
38	126	94.7	27	7	ADC22452
39	126	94.7	27	7	ADH76188
40	126	94.7	27	7	ADH76182
41	126	94.7	27	8	ADH89702
42	126	94.7	27	8	ADI52969
43	126	94.7	27	8	ADLI4690
44	126	94.7	27	8	ADLI4684
45	126	94.7	27	8	ADR31976

Adm97018 Botulinum
Ado43344 Transport
Ado80842 Synthetic
Adq60192 Galanin/M
Adr00873 Transport
Adsi17605 Membrane
Adk39821 PNA molec
Adk39821 PNA molec
Adh89695 Cell pene
Adh89696 Cell pene
Ado25261 Transpor
Adc22458 Protein-d
Adc22452 Protein-d
Adh76188 Transduct
Adh76182 Transduct
Adh89702 Cell pene
Adi52969 Polysacch
Adli4690 Cardiant
Adli4684 Cardiant
Adr31976 Heat shoc

XX SQ Sequence 27 AA; Query Match 100.0%; Score 133; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||
DB 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||

RESULT 2
AAB17999
ID AAB17999 standard; peptide; 27 AA.
XX
AC AAB17999;
XX
DT 31-OCT-2000 (first entry)
XX
DE Membrane transporting peptide sequence SEQ ID NO:1111.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO2000024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Disclosure; Page 602; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 133; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||
DB 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||

RESULT 3
AAB22024
ID AAB22024 standard; peptide; 27 AA.
XX
AC AAB22024;
XX
DT 08-JAN-2001 (first entry)
XX
DE Membrane penetrating peptide #1.
XX
KW Cystic fibrosis transmembrane conductance regulator; CFTR; CF;
KW chloride channel; membrane penetrating peptide.
XX
OS Unidentified.
XX
PN WO2000050591-A1.
XX
PD 31-AUG-2000.
XX
PF 24-FEB-2000; 2000WO-US004642.
XX
PR 24-FEB-1999; 99US-0121495P.
XX
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Adams LM, Davis PB, Ma J;
XX
DR WPI; 2000-572090/53.
XX
PT Polypeptide useful for enhancing the open probability of cystic fibrosis
PT transmembrane conductance regulator chloride channel in cystic fibrosis
PT patients having minimally active mutant protein.
XX
PS Claim 5; Page 31; 35pp; English.
XX
CC Defects in the cystic fibrosis transmembrane conductance regulator
CC (CFTR), are associated with cystic fibrosis (CF). CFTR is a chloride
CC channel located in the apical membrane of epithelial cells. The present
CC invention relates to peptide fragments of human CFTR (see AAB22022 and
CC AAB22023), which are useful for CF therapy, in that they can activate and
CC open a CFTR protein by the formation of a cAMP regulated chloride
CC channel. The present peptide is a membrane penetrating peptide, which can
CC be fused onto the AAB22022 and AAB22023 peptides. The present peptide can
CC be used to facilitate the uptake of the AAB22022 and AAB22023 peptides by
CC target cells
XX
SQ Sequence 27 AA;

Query Match 100.0%; Score 133; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||
DB 1 GWTLSAGYLLGKINKALAAALAKKIL 27
|||||

RESULT 4
AAB29575
ID AAB29575 standard; protein; 27 AA.
XX
AC AAB29575;
XX
DT 15-FEB-2001 (first entry)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:04:32 ; Search time 143.791 Seconds
(without alignments)
77.948 Million cell updates/sec

Title: US-10-071-512A-3
Perfect score: 133
Sequence: 1 GWTLSAGYLLGKINKALAKKIL 27

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	133	100.0	27	10	US-09-948-193-18
2	133	100.0	27	10	US-09-295-189-5
3	133	100.0	27	12	US-09-777-560-12
4	133	100.0	27	14	US-10-071-512A-3
5	133	100.0	27	14	US-10-252-012-4
6	133	100.0	27	14	US-10-156-570A-25
7	133	100.0	27	14	US-10-201-394A-21
8	133	100.0	27	14	US-10-201-389A-21
9	133	100.0	27	15	US-10-144-549-16
10	133	100.0	27	15	US-10-357-529-9
11	133	100.0	27	15	US-10-232-410-13
12	133	100.0	27	10	US-09-948-193-18
13	133	100.0	27	10	US-09-295-189-5
14	133	100.0	27	12	US-09-777-560-12
15	133	100.0	27	14	US-10-071-512A-3
16	133	100.0	27	14	US-10-252-012-4
17	133	100.0	27	14	US-10-156-570A-25
18	133	100.0	27	14	US-10-201-394A-21
19	133	100.0	27	14	US-10-201-389A-21
20	133	100.0	27	15	US-10-144-549-16
21	133	100.0	27	15	US-10-357-529-9
22	133	100.0	27	15	US-10-232-410-13

12	133	100.0	27	15	US-10-609-217-1109	Sequence 1109, Ap
13	133	100.0	27	15	US-10-632-388-1109	Sequence 1109, Ap
14	133	100.0	27	15	US-10-357-826A-3	Sequence 3, Appli
15	133	100.0	27	15	US-10-651-723-1109	Sequence 1109, Ap
16	133	100.0	27	15	US-10-645-761-1109	Sequence 1109, Ap
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18	133	100.0	27	15	US-10-666-696-1109	Sequence 1109, Ap
19	133	100.0	27	15	US-10-653-048-1109	Sequence 1109, Ap
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23	133	100.0	27	16	US-10-185-860A-4	Sequence 4, Appli
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25	133	100.0	27	16	US-10-634-447-5	Sequence 5, Appli
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28	133	100.0	27	17	US-10-826-966-514	Sequence 514, App
29	133	100.0	27	17	US-10-795-081A-12	Sequence 12, Appli
30	133	100.0	27	17	US-10-930-313-56	Sequence 56, Appli
31	133	100.0	27	18	US-10-645-784-1109	Sequence 1109, Ap
32	133	100.0	27	18	US-10-694-243-8	Sequence 8, Appli
33	133	100.0	27	18	US-10-972-963-8	Sequence 8, Appli
34	133	100.0	27	18	US-10-353-902-7	Sequence 7, Appli
35	133	100.0	27	18	US-10-878-175B-35	Sequence 35, Appli
36	133	100.0	27	20	US-11-001-674-12	Sequence 12, Appli
37	127	95.5	27	17	US-10-700-971C-3	Sequence 3, Appli
38	126	94.7	27	14	US-10-226-956-283	Sequence 283, App
39	126	94.7	27	14	US-10-226-956-289	Sequence 289, App
40	126	94.7	27	14	US-10-211-088-301	Sequence 301, App
41	126	94.7	27	14	US-10-211-088-307	Sequence 307, App
42	126	94.7	27	14	US-10-405-339-30	Sequence 30, Appli
43	116.5	87.6	26	9	US-09-785-802A-12	Sequence 12, Appli
44	116.5	87.6	26	10	US-09-965-876A-4	Sequence 4, Appli
45	116.5	87.6	26	14	US-10-077-555-10	Sequence 10, Appli

ALIGNMENTS

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; Sequence 18, Application US/09948193
; Publication No. US20030027335A1
; GENERAL INFORMATION:
; APPLICANT: Jo, Daewoong
; TITLE OF INVENTION: Genome Engineering by Cell-Permeable DNA
; FILE REFERENCE: 22000.0109U2
; CURRENT APPLICATION NUMBER: US/09/948,193
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/230,690
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description: Transportan
US-09-948-193-18

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Db 1 GWTLSAGYLLGKINKALAKKIL 27

RESULT 2

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; Sequence 5, Application US/09295189
; Publication No. US20030083273A1
; GENERAL INFORMATION:
; APPLICANT: Woolf, Tod M.
; TITLE OF INVENTION: Improved Antisense Oligomers
; FILE REFERENCE: SRI-004
; CURRENT APPLICATION NUMBER: US/09/295,189
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-295-189-5

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 3
US-09-777-560-12
; Sequence 12, Application US/09777560
; Publication No. US20050130884A1
; GENERAL INFORMATION:
; APPLICANT: BRANDT, CURTIS R.
; APPLICANT: BULTMANN, HERMANN
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE ANTIVIRAL PEPTIDES AND METHODS
; TITLE OF INVENTION: OF THEIR USE
; FILE REFERENCE: 032026-0460
; CURRENT APPLICATION NUMBER: US/09/777,560
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/184,057
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/180,823
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-777-560-12

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-071-512A-3
; Sequence 3, Application US/10071512A
; Publication No. US20030031655A1
; GENERAL INFORMATION:
; APPLICANT: Woolf, Tod M.
; TITLE OF INVENTION: METHODS OF LIGHT ACTIVATED RELEASE OF LIGANDS FROM
; TITLE OF INVENTION: ENDOSOMES

; FILE REFERENCE: SRI-014
; CURRENT APPLICATION NUMBER: US/10/071,512A
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 60/267272
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 7
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; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-071-512A-3

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RESULT 5
US-10-252-012-4
; Sequence 4, Application US/10252012
; Publication No. US20030100501A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Pamela B.
; TITLE OF INVENTION: OAN2NEG2 AN ACTIVATOR OF WILD TYPE AND MUTANT CFTR CHLORIDE CHANNEL
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 03037.00012
; CURRENT APPLICATION NUMBER: US/10/252,012
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
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US-10-252-012-4

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Best Local Similarity 100.0%; Pred. No. 2.7e-12;
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RESULT 6
US-10-156-570A-25
; Sequence 25, Application US/10156570A
; Publication No. US20030125242A1
; GENERAL INFORMATION:
; APPLICANT: ROSENECKER, JOSEPH
; APPLICANT: RITTER, WOLFGANG
; APPLICANT: RUDOLPH, CARSTEN MARTIN
; APPLICANT: PLANK, CHRISTIAN
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR
; TITLE OF INVENTION: LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS
; TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: INTO CELLS
; FILE REFERENCE: VOS-35
; CURRENT APPLICATION NUMBER: US/10/156,570A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: PCT/EP00/11690
; PRIOR FILING DATE: 2000-11-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25

GenCore version 5.1.6
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Run on: October 4, 2005, 14:01:01 ; Search time 436.395 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	133	100.0	27	1	PCT-US02-30094-4	Sequence 4, Appl
3	133	100.0	27	1	PCT-US03-25567-64	Sequence 64, Appl
4	133	100.0	27	1	PCT-US03-28092-24	Sequence 24, Appl
5	133	100.0	27	1	PCT-US03-33801-8	Sequence 8, Appl
6	133	100.0	27	1	PCT-US03-34424-29	Sequence 29, Appl
7	133	100.0	27	1	PCT-US03-34686-26	Sequence 26, Appl
8	133	100.0	27	1	PCT-US04-11195-112	Sequence 112, Appl
9	133	100.0	27	1	PCT-US04-35137-8	Sequence 8, Appl
10	133	100.0	27	1	PCT-US99-25044-111	Sequence 111, Appl
11	133	100.0	27	16	US-09-295-189-5	Sequence 5, Appl
12	133	100.0	27	19	US-09-563-286B-1109	Sequence 1109, Appl
13	133	100.0	27	19	US-09-563-286C-1109	Sequence 1109, Appl
14	133	100.0	27	22	US-09-777-560-12	Sequence 12, Appl
15	133	100.0	27	24	US-09-914-213-4	Sequence 4, Appl
16	133	100.0	27	24	US-09-948-193-18	Sequence 18, Appl
17	133	100.0	27	26	US-10-071-512A-3	Sequence 3, Appl
18	133	100.0	27	27	US-10-156-570A-25	Sequence 25, Appl
19	133	100.0	27	27	US-10-185-860A-4	Sequence 4, Appl
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21	133	100.0	27	28	US-10-201-394A-21	Sequence 21, Appl
22	133	100.0	27	28	US-10-232-410-13	Sequence 13, Appl
23	133	100.0	27	28	US-10-252-012-4	Sequence 4, Appl
24	133	100.0	27	28	US-10-261-161-24	Sequence 24, Appl
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26	133	100.0	27	29	US-10-357-529-9	Sequence 9, Appl
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28	133	100.0	27	30	US-10-427-160A-21	Sequence 21, Appl
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35	133	100.0	27	32	US-10-651-723-1109	Sequence 1109, Appl
36	133	100.0	27	32	US-10-653-048-1109	Sequence 1109, Appl
37	133	100.0	27	32	US-10-666-896-1109	Sequence 1109, Appl
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39	133	100.0	27	33	US-10-743-381-4	Sequence 4, Appl
40	133	100.0	27	33	US-10-751-380-20	Sequence 20, Appl
41	133	100.0	27	33	US-10-757-803-514	Sequence 514, Appl
42	133	100.0	27	33	US-10-780-447-21	Sequence 21, Appl
43	133	100.0	27	33	US-10-795-881A-12	Sequence 12, Appl
44	133	100.0	27	34	US-10-826-966-514	Sequence 514, Appl
45	133	100.0	27	34	US-10-874-920-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
PCT-US02-22324-21
; Sequence 21, Application PC/TUS0222324
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Beigelman, Leonid
; APPLICANT: Azharyev, Alex
; APPLICANT: Azharyeva, Elena
; APPLICANT: Antopolsky, Maxim
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID PEPTIDE CONJUGATES
; FILE REFERENCE: MBH01-895-B (600/024)
; CURRENT APPLICATION NUMBER: PCT/US02/22324
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ IDS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic peptide
PCT-US02-22324-21

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 2
PCT-US02-30094-4
; Sequence 4, Application PC/TUS0230094
; GENERAL INFORMATION:
; APPLICANT: Davis, Pamela B.
; TITLE OF INVENTION: QAN2NEG2 AN ACTIVATOR OF WILD TYPE AND MUTANT CFTR CHLORIDE CHANNEL
; FILE REFERENCE: ACTIVITY
; CURRENT APPLICATION NUMBER: PCT/US02/30094
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: homo sapiens
PCT-US02-30094-4

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Best Local Similarity 100.0%; Pred. No. 2.4e-13;
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RESULT 3
PCT-US03-25567-64
; Sequence 64, Application PC/TUS0325567
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Novel Peptide-Conjugated Oligomeric Compounds
; FILE REFERENCE: ISIS-5244
; CURRENT APPLICATION NUMBER: PCT/US03/25567
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/222,595
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
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Best Local Similarity 100.0%; Pred. No. 2.4e-13;
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RESULT 4
PCT-US03-28092-24
; Sequence 24, Application PC/TUS0328092
; GENERAL INFORMATION:
; APPLICANT: Allergan, Inc.
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: 17511 (BOT)
; CURRENT APPLICATION NUMBER: PCT/US03/28092
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US03-28092-24

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Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GWTLSAGYLLGKINKLALAALAKKIL 27
Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 5
PCT-US03-33801-8
; Sequence 8, Application PC/TUS0333801
; GENERAL INFORMATION:
; APPLICANT: GEORGIA TECH RESEARCH CORPORATION
; APPLICANT: EMORY UNIVERSITY
; TITLE OF INVENTION: MULTIFUNCTIONAL MAGNETIC NANOPARTICLE PROBES FOR INTRACELLULAR MOLECULAR IMAGING AND MONITORING
; FILE REFERENCE: 17625-0059
; CURRENT APPLICATION NUMBER: PCT/US03/33801
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: 60/421,361
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
PCT-US03-33801-8

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GWTLSAGYLLGKINKLALAALAKKIL 27
Db 1 GWTLSAGYLLGKINKLALAALAKKIL 27

RESULT 6
PCT-US03-34424-29
; Sequence 29, Application PC/TUS0334424
; GENERAL INFORMATION:
; APPLICANT: The Center For Blood Research, Inc., et al.
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION USING RNA INTERFERING AGENTS
; FILE REFERENCE: CBN-007PC
; CURRENT APPLICATION NUMBER: PCT/US03/34424
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,419
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 31
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:03:57 ; Search time 64.0465 Seconds
(without alignments)
73.895 Million cell updates/sec

Title: US-10-071-512A-3

Perfect score: 133

Sequence: 1 GWTLSAGYLLGKINLKALALAKKIL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286997 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New.*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	133	100.0	27	1	PCT-US04-35009-6
2	133	100.0	27	1	PCT-US05-01771-7
3	133	100.0	27	1	PCT-US05-05458-12
4	133	100.0	27	1	PCT-US04-36200-10
5	133	100.0	27	1	PCT-US04-40119-12
6	133	100.0	27	1	PCT-US04-06911A-12
7	133	100.0	27	6	US-10-930-313-56
8	133	100.0	27	6	US-10-156-570B-25
9	133	100.0	27	6	US-10-878-175B-35
10	133	100.0	27	6	US-10-201-389B-21
11	133	100.0	27	6	US-10-535-780-4
12	133	100.0	27	6	US-10-923-112A-35
13	133	100.0	27	7	US-11-041-103-7
14	133	100.0	27	7	US-11-109-015-2
15	133	100.0	27	7	US-11-001-674-12
16	133	100.0	27	7	US-11-067-092A-7
17	133	100.0	27	7	US-11-126-562-9
18	133	100.0	27	7	US-11-126-551-11
19	133	100.0	27	7	US-11-049-636-16
20	133	100.0	27	7	US-11-112-950-3
21	133	100.0	27	7	US-11-107-371-3
22	133	100.0	27	8	US-60-654-981-11
23	133	100.0	27	8	US-60-654-981-23
24	133	100.0	27	8	PCT-US05-16746-3
25	127	95.5	27	1	PCT-US04-35009-6

Sequence 3, Appli
Sequence 283, App
Sequence 289, App
Sequence 35, Appl
Sequence 5, Appli
Sequence 28, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 27, Appl
Sequence 13, Appl

26 127 95.5 27 6 US-10-700-971C-3
27 126 94.7 27 7 US-11-078-256-283
28 126 94.7 27 7 US-11-078-256-283
29 116.5 87.6 26 6 US-10-991-286A-35
30 116.5 87.6 26 6 US-10-985-425-5
31 116.5 87.6 26 6 US-10-899-912A-28
32 116.5 87.6 26 7 US-11-016-542-7
33 112 84.2 25 7 US-11-126-562-11
34 112 84.2 25 7 US-11-126-551-11
35 112 84.2 25 8 US-60-654-981-26
36 111 83.5 24 7 US-11-126-562-10
37 111 83.5 24 7 US-11-126-551-10
38 111 83.5 24 8 US-60-654-981-24
39 97 72.9 21 1 PCT-US05-18995-18
40 97 72.9 21 1 PCT-US04-06911A-13
41 97 72.9 21 7 US-11-126-562-12
42 97 72.9 21 7 US-11-126-551-12
43 97 72.9 21 7 US-11-141-725-15
44 97 72.9 21 8 US-60-654-981-27
45 90 67.7 22 7 US-11-126-562-13

ALIGNMENTS

RESULT 1

PCT-US04-35009-6
; Sequence 6, Application PC/TUS0435009
; GENERAL INFORMATION:
; APPLICANT: Wake Forest University Health Sciences
; APPLICANT: Payne, R. Mark
; TITLE OF INVENTION: NON-VIRAL DELIVERY OF COMPOUNDS TO THE MITOCHONDRIA
; FILE REFERENCE: 9151-37W0
; CURRENT APPLICATION NUMBER: PCT/US04/35009
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,892
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic PTD sequence
PCT-US04-35009-6

Query Match 100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GWTLSAGYLLGKINLKALALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALALAKKIL 27

RESULT 2

PCT-US05-01771-7
; Sequence 7, Application PC/TUS0501771
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; APPLICANT: Bao, Gang
; APPLICANT: Nitin, Nitin
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection
; FILE REFERENCE: 820701-2820
; CURRENT APPLICATION NUMBER: PCT/US05/01771
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/179,730
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/300,672
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/303,258
; PRIOR FILING DATE: 2001-07-03

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; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
PCT-US05-01771-7

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 3
PCT-US05-05458-12
; Sequence 12, Application PC/TUS050505458
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: DFN-058PC
; CURRENT APPLICATION NUMBER: PCT/US05/05458
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: 60/548,139
; PRIOR FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
PCT-US05-05458-12

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 4
PCT-US04-36200-10
; Sequence 10, Application PC/TUS0436200
; GENERAL INFORMATION:
; APPLICANT: THE CBR INSTITUTE FOR BIOMEDICAL RESEARCH, INC.
; APPLICANT: LIEBERMAN, JUDY
; APPLICANT: HAMAR, PETER
; TITLE OF INVENTION: METHODS FOR TREATING AND PREVENTING ISCHEMIA-REPERFUSION
; FILE REFERENCE: 033393-55221
; CURRENT APPLICATION NUMBER: PCT/US04/36200
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: 60/516,172
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT

; PRIOR APPLICATION NUMBER: 60/538,381
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/538,382
; PRIOR FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
PCT-US05-01771-7

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 5
PCT-US04-40119-12
; Sequence 12, Application PC/TUS0440119
; GENERAL INFORMATION:
; APPLICANT: BRANDT, CURTIS R.
; APPLICANT: BULTMANN, HERMANN
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR INDUCING CELLULAR RESISTANCE
; FILE REFERENCE: 032026-0827
; CURRENT APPLICATION NUMBER: PCT/US04/40119
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: 60/526,252
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
PCT-US04-40119-12

Query Match      100.0%; Score 133; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALAALAKKIL 27
Db 1 GWTLSAGYLLGKINLKALAALAKKIL 27

RESULT 6
PCT-US04-06911A-12
; Sequence 12, Application PC/TUS0406911A
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS
; FILE REFERENCE: 411.35629AP3
; CURRENT APPLICATION NUMBER: PCT/US04/06911A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/451,980
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 09/865,281
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Synthesized peptide
PCT-US04-06911A-12
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:20:28 ; Search time 31.3953 Seconds
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82.746 Million cell updates/sec

Title: US-10-071-512A-3
Perfect score: 133
Sequence: 1 GWTLSAGYLLGKLNKALAAKIL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	50.4	29	S17147	galanin - chicken
2	67	50.4	99	S34301	galanin - mouse
3	67	50.4	123	RHBOG	galanin precursor
4	67	50.4	123	RHHUN	galanin precursor
5	67	50.4	123	RHPGN	galanin precursor
6	67	50.4	124	RHRTN	galanin precursor
7	67	50.4	124	JCS480	galanin precursor
8	61	45.9	14	QMWAVV	mastoparan - yello
9	57	42.9	14	QMVHMM	mastoparan M - hor
10	55	41.4	558	T47505	hypothetical prote
11	54	40.6	14	JN0389	histamine-releasin
12	52	39.1	516	T47509	probable transport
13	52	39.1	548	T47510	probable transport
14	52	39.1	555	T47512	probable transport
15	51	38.3	14	QMVHP2	mastoparan C - Eur
16	51	38.3	558	T47508	probable transport
17	50	37.6	557	T47506	hypothetical prote
18	50	37.6	609	T00904	hypothetical prote
19	50	37.6	1260	T04440	hypothetical prote
20	49.5	37.2	167	AG3384	3-dehydroquinat
21	49	36.8	206	G83854	hypothetical prote
22	49	36.8	299	F90741	hypothetical prote
23	49	36.8	299	A85592	hypothetical prote
24	49	36.8	302	T09321	EPLF2 protein - hu
25	49	36.8	308	H64819	formate acetyltran
26	49	36.8	568	E70962	probable fadE4 pro
27	49	36.8	752	KXRTC1	proprotein convert
28	49	36.8	753	KXHCUC1	proprotein convert
29	49	36.8	753	KXMSC1	proprotein convert

30	49	36.8	753	2	S59959	proprotein convert
31	48.5	36.5	426	2	A11177	3-hydroxy-3-methyl
32	48	36.1	219	2	G90602	chromate transport
33	47.5	35.7	426	2	AE1535	3-hydroxy-3-methyl
34	47	35.3	105	1	RSUC12	ribosomal protein
35	47	35.3	190	2	D75006	hypothetical prote
36	47	35.3	326	2	AB2810	hypothetical prote
37	47	35.3	326	2	E97588	bifunctional carbo
38	47	35.3	438	2	C72006	conserved hypotet
39	47	35.3	438	2	F86619	CT372 hypothetical
40	47	35.3	2971	2	T08026	hypothetical prote
41	46.5	35.0	226	2	C69760	amino acid ABC tra
42	46.5	35.0	350	2	JN0621	G protein-coupled
43	46.5	35.0	374	2	F81693	iron-sulfur cofact
44	46	34.6	122	2	H70791	hypothetical prote
45	46	34.6	201	2	AG0793	Ais protein (impor

ALIGNMENTS

RESULT 1
S17147
galanin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S17147
R:Norberg, A.; Sillard, R.; Carlquist, M.; Joernvall, H.; Mutt, V.
PEBS Lett. 288, 151-153, 1991
A>Title: Chemical detection of natural peptides by specific structures. Isolation of chi
A:Reference number: S17147; MUID:91348254; PMID:1715289
A:Accession: S17147
A:Molecule type: protein
A:Status: preliminary
A:Residues: 1-29 <NOR>
A:Cross-references: UNIPROT:P30802
C:Superfamily: galanin

Query Match 50.4%; Score 67; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
Db 1 GWTLSAGYLLG 12
|||||

RESULT 2
S34301
galanin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34301
R:Land, T.; Lundqvist, J.; Bartfai, T.
Submitted to the EMBL Data Library, June 1993
A:Description: Cloning of mouse galanin/cDNA.
A:Reference number: S34301
A:Accession: S34301
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <LAN>
A:Cross-references: UNIPROT:P47212; EMBL:Z23069; NID:g312338; PIDN:CAA80610.1; PID:g312338

Query Match 50.4%; Score 67; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
Db 8 GWTLSAGYLLG 19
|||||

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RESULT 3
RHBOG
galanin precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S01011; I46971
R:Roekaeus, A.; Carlquist, M.
FBBS Lett. 234, 400-406, 1988
A>Title: Nucleotide sequence analysis of cDNAs encoding a bovine galanin precursor protein
A:Reference number: S01011; MUID:88271665; PMID:2455659
A:Accession: S01011
A:Molecule type: mRNA
A:Residues: 1-123 <ROB>
A:Cross-references: UNIPROT:P11242; EMBL:X12582; NID:G376; PIDN:CAA31094.1; PID:G377
A>Note: the authors translated the codon ACT for residue 95 as Tyr
R:Anouar, Y.; MacArthur, L.; Cohen, J.; Iacangelo, A.L.; Eiden, L.E.
J. Biol. Chem. 269, 6823-6831, 1994
A>Title: Identification of a TPA-responsive element mediating preferential transactivation
A:Reference number: I46971; MUID:94165083; PMID:7509811
A:Accession: I46971
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-27 <ANO>
A:Cross-references: GB:S68957; NID:G545739; PIDN:AAD14027.1; PID:G4261727
C:Superfamily: galanin
C:Keywords: amidated carboxyl end; hormone; intestine; neuropeptide
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-32/Domain: amino-terminal propeptide #status predicted <PRO>
F:33-61/Product: galanin #status predicted <MAT>
F:62-123/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:61/Modified site: amidated carboxyl end (Ala) (amide in mature form from following gly

Query Match 50.4%; Score 67; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
| | | | | | | | | |
DB 33 GWTLSAGYLLG 44

RESULT 4
RHUN
galanin precursor [validated] - human
N:Contains: galanin; galanin mRNA associated peptide (GMAP)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A49353; A61116; A49154; A41630; S15931
R:Evans, H.; Baumgartner, M.; Shine, J.; Herzog, H.
Genomics 18, 473-477, 1993
A>Title: Genomic organization and localization of the gene encoding human preprogalanin.
A:Reference number: A49353; MUID:94140342; PMID:7508413
A:Accession: A49353
A:Molecule type: DNA
A:Residues: 1-45 <EV2>
A:Cross-references: UNIPROT:P22466; GB:L11114; NID:G306764; PIDN:AAA18248.1; PID:G488849
A>Note: neither nucleotide sequence nor translation is complete
R:Evans, H.F.; Shine, J.
Endocrinology 129, 1682-1684, 1991
A>Title: Human galanin: molecular cloning reveals a unique structure.
A:Reference number: A61116; MUID:91339793; PMID:1714839
A:Accession: A61116
A:Molecule type: mRNA
A:Residues: 1-123 <EVA>
R:McKnight, G.L.; Karlsson, A.E.; Kowalyk, S.; Mathewes, S.L.; Sheppard, P.O.; O'Hara, P.
Diabetes 41, 82-87, 1992
A>Title: Sequence of human galanin and its inhibition of glucose-stimulated insulin secretion
A:Reference number: A49154; MUID:92090542; PMID:1370155
A:Accession: A49154
A:Molecule type: mRNA
A:Residues: 17-123 <MCK>
A:Cross-references: GB:JMW7140; NID:G190411; PIDN:AAA60178.1; PID:G190412
A>Note: sequence extracted from NCBI backbone (NCBIN:71608, NCBIP:71609)

```

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R:Schmidt, W.E.; Kratzin, H.; Eckart, K.; Dreys, D.; Mundkowski, G.; Clemens, A.; Katson
Proc. Natl. Acad. Sci. U.S.A. 88, 11435-11439, 1991
A>Title: Isolation and primary structure of pituitary human galanin, a 30-residue nonam
A:Reference number: A41630; MUID:92107965; PMID:1722333
A:Accession: A41630
A:Molecule type: protein
A:Residues: 33-62 <SCH>
A>Note: sequence extracted from NCBI backbone
R:Bersani, M.; Johnsen, A.H.; Hojrup, P.; Dunning, B.E.; Andreassen, J.J.; Holst, J.J.
FBBS Lett. 283, 189-194, 1991
A>Title: Human galanin: primary structure and identification of two molecular forms.
A:Reference number: S15831; MUID:91257299; PMID:1710578
A:Accession: S15831
A:Molecule type: protein
A:Residues: 33-62 <BER>
A>Note: a form containing only the first nineteen residues of this sequence was also fou
C:Comment: This peptide causes smooth muscle contraction in the gastrointestinal tract a
C:Comment: This peptide in human differs from the pig, rat, and bovine forms by the absen
C:Genetics:
A:Gene: GDB:GALN
A:Cross-references: GDB:I41567; OMIM:137035
A:Map position: 11q13.3-11q13.5
C:Superfamily: galanin
C:Keywords: hormone; intestine; neuropeptide
F:1-23/Domain: signal sequence #status predicted <SIG>
F:33-62/Product: galanin #status experimental <MAT>
F:65-123/Product: galanin mRNA associated peptide (GMAP) #status predicted <RMAT>

Query Match 50.4%; Score 67; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLG 12
| | | | | | | | | |
DB 33 GWTLSAGYLLG 44

RESULT 5
RHFGN
galanin precursor - pig
N:Contains: preprogalanin, 7-residue amino end-extended form; preprogalanin, 9-residue a
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Sep-1988 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A23540; J00002; A49161
R:Roekaeus, A.; Brownstein, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 6287-6291, 1986
A>Title: Construction of a porcine adrenal medullary cDNA library and nucleotide sequen
A:Reference number: A23540; MUID:86313566; PMID:2428032
A:Accession: A23540
A:Molecule type: mRNA
A:Residues: 1-123 <ROB>
A:Cross-references: UNIPROT:P07480; GB:M13826; NID:G164605; PIDN:AAA31097.1; PID:G164606
R:Tatemoto, K.; Roekaeus, A.; Jornvall, H.; McDonald, T.J.; Mutt, V.
FBBS Lett. 164, 124-128, 1983
A>Title: Galanin: a novel biologically active peptide from porcine intestine.
A:Reference number: J00002; MUID:84085072; PMID:6197320
A:Accession: J00002
A:Molecule type: protein
A:Residues: 33-61 <TAT>
A:Experimental source: intestine
R:Bersani, M.; Thim, L.; Rasmussen, T.N.; Holst, J.J.
Endocrinology 129, 2693-2698, 1991
A>Title: Galanin and galanin extended at the N-terminus with seven and nine amino acids
A:Reference number: A49161; MUID:92037394; PMID:1718731
A:Accession: A49161
A:Molecule type: protein
A:Residues: 1-123 <BER>
A:Experimental source: adrenal medulla
A>Note: sequence extracted from NCBI backbone (NCBIP:63296)
C:Comment: This peptide contracts smooth muscle preparations from rat and causes a mild
C:Superfamily: galanin
C:Keywords: amidated carboxyl end; hormone; intestine; neuropeptide
F:1-23/Domain: signal sequence #status predicted <SIG>

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 14:08:33 ; Search time 145.674 Seconds
(without alignments)
94.911 Million cell updates/sec

Title: US-10-071-512A-3

Perfect score: 133

Sequence: 1 GWTLSAGVLLGKLNKALAAKIL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	69.5	52.3	115	1 GALP RAT
2	69	51.9	29	1 GALA_ONCMY
3	69	51.9	55	2 Q8VIL6
4	69	51.9	115	2 Q8SQD7
5	69	51.9	116	1 GALP_HUMAN
6	69	51.9	117	2 Q810H5
7	69	51.9	120	1 GALP_PIG
8	68	51.1	58	2 Q7ZT95
9	68	51.1	81	2 Q7ZT97
10	68	51.1	95	2 Q7ZT92
11	68	51.1	118	2 Q7ZT94
12	67	50.4	26	2 Q7ZT98
13	67	50.4	29	1 GALA_ALLMI
14	67	50.4	29	1 GALA_AMICA
15	67	50.4	29	1 GALA_CHICK
16	67	50.4	29	1 GALA_RANRI
17	67	50.4	29	1 GALA_SHEEP
18	67	50.4	50	2 Q7ZT89
19	67	50.4	55	2 Q8SQD6
20	67	50.4	81	2 Q7ZT96
21	67	50.4	117	1 GALA_COTJA
22	67	50.4	120	2 Q7ZT91
23	67	50.4	123	1 GALA_BOVIN
24	67	50.4	123	1 GALA_HUMAN
25	67	50.4	123	1 GALA_PIG
26	67	50.4	124	1 GALA_MOUSE
27	67	50.4	124	1 GALA_RAT
28	67	50.4	142	2 Q7ZT93
29	67	50.4	144	2 Q7ZT90
30	67	50.4	14	1 MAST_VESLE
31	57	42.9	14	1 MAST_VESMA

32 55 41.4 558 2 Q9M1E2
33 54 40.6 14 1 MAST_VESOR
34 54 40.6 375 2 Q6L3J3
35 53.5 40.2 539 2 Q7NTF4
36 52 39.1 516 2 Q9M174
37 52 39.1 548 2 Q8GZ59
38 52 39.1 548 2 Q9M173
39 52 39.1 555 2 Q9M171
40 52 39.1 774 2 Q9YHY5
41 52 39.1 1109 2 Q6BZH6
42 51.5 38.7 589 2 Q7P6I6
43 51 38.3 14 1 MAST_VESCR
44 51 38.3 309 2 Q9AXI9
45 51 38.3 558 2 Q8GYF8

ALIGNMENTS

RESULT 1

ID GALP RAT STANDARD; PRT; 115 AA.
AC Q9QXG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galanin-like peptide precursor.
OS Name=Galp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069685; PubMed=10601261; DOI=10.1074/jbc.274.52.37041;
RA Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,
RA Kitada C., Kurokawa T., Onda H., Fujino M.;
RT "Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
RT from porcine hypothalamus";
RL J. Biol. Chem. 274:37041-37045(1999).
CC - SUBCELLULAR LOCATION: Secreted.
CC - SIMILARITY: Belongs to the galanin family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL; AF188491; AAF19723.1; --
CC InterPro; IPR008174; Galanin.
CC Pfam; PF01296; Galanin; 1.
CC PROSITE; PS00861; GALANIN; 1.
CC Cleavage on pair of basic residues; Hormone; Neuropeptide; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 83 Galanin-like peptide.
FT PROPEP 86 115 By similarity.
SQ SEQUENCE 115 AA; 12599 MW; 00BD3A2336AD06C5 CRC64;

Query Match 52.3%; Score 69.5; DB 1; Length 115;
Best Local Similarity 57.7%; Pred. No. 0 032;

Matches 15; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 GWTLSAGVLLGKI-NLKALAAKX 25

||||| : : : : :
Db 32 GWTLSAGVLLGPVLHLSKANQGRK 57

RESULT 2

ID GALA_ONCMY STANDARD; PRT; 29 AA.
31

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AC P47213;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galanin.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95164756; PubMed=7532194;
RA Anglade I., Wang Y., Jensen J., Framu G., Kah O., Conlon J.M.;
RT "Characterization of trout galanin and its distribution in trout brain
RT and pituitary.";
RL J. Comp. Neurol. 350:63-74(1994).
CC -!- FUNCTION: Contracts smooth muscle of the gastrointestinal and
CC genitourinary tract, regulates growth hormone release, modulates
CC insulin release, and may be involved in the control of adrenal
CC secretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the galanin family.
DR InterPro; IPR008174; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR PRODOM; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Neuropeptide.
FT MOD_RES 29 29 Alanine amide.
SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 51.9%; Score 69; DB 1; Length 29;
Best Local Similarity 56.0%; Pred. No. 0.011;
Matches 14; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKINLKALALAKK 25
Db ||||| :
1 GWTLSAGYLLGPHGIDGHTLSDK 25

RESULT 3
QSVIL6 PRELIMINARY; PRT; 55 AA.
ID Q8VIL6
AC Q8VIL6;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Galanin-like peptide (Fragment).
GN Name=Galp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21569989; PubMed=11713207; DOI=10.1210/en.142.12.5140;
RA Jureus A., Cunningham M.J., Li D., Johnson L.L., Krasnow S.M.,
RA Tekemichael D.N., Clifton D.K., Steiner R.A.;
RT "Distribution and Regulation of Galanin-Like Peptide (GALP) in the
RT Hypothalamus of the Mouse.";
RL Endocrinology 142:5140-5144(2001).
DR EMBL; AF426450; AAL32205.1; -.
DR MGI; MGI:2663979; Galp.
DR GO; GO:0005102; P:receptor binding; TAS.
DR Pfam; PF01296; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
FT NON_TER 1 1
FT NON_TER 55 55
SQ SEQUENCE 55 AA; 5785 MW; 995DF6B2C7977D2 CRC64;

Query Match 51.9%; Score 69; DB 2; Length 55;
Best Local Similarity 85.7%; Pred. No. 0.038;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GWTLSAGYLLGKI 14
Db ||||| :
32 GWTLSAGYLLGPV 45

RESULT 5
GALP_HUMAN STANDARD; PRT; 116 AA.
ID GALP_HUMAN
AC Q9UBC7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galanin-like peptide precursor.
GN Name=GALP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069685; PubMed=10601261; DOI=10.1074/jbc.274.52.37041;
RA Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,
RA Kitada C., Kurokawa T., Onda H., Fujino M.;
RT "Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
RT from porcine hypothalamus.";
RL J. Biol. Chem. 274:37041-37045(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the galanin family.

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